

PerCore version 4.5
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On nucleic nucleic secret, using sw model

March 14, 2002, 15:21:00 : Search time 151.71 seconds

(without alignments)
103.006 Million cell updates/sec

115-(9-786) 109-4

Sequence: 1 ctatggtatctctccggtatc.....ccatggccatattctctaat 59

Find table: ICHNCTV_006

 $\text{Gap}_{\text{top}} = 0.3$, $\text{Gap}_{\text{ext}} = 1.0$

Searched: 351203 seqs, 113238999 residues

total number of hits satisfying chosen parameters: 702406

Maximum DB seq length: 200000000000

[illegible]

Listing first 45 summaries

Database :

[illegible]

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB	ID	Description
1	26.9	38.8	6.95	2	05-08-806-410-2	Sequence 3, Appl Sequence 37, Appl
2	26.8	38.8	1.05	2	05-08-806-410-27	Sequence 37, Appl
3	24	34.8	11.91	2	05-08-968-751-5	Sequence 5, Appl
4	24	34.8	1.959	4	05-09-201-641-1	Sequence 1, Appl
5	23.8	44.3	36.750	3	05-09-315-404-1	Sequence 1, Appl
6	23.4	31.3	26.05	2	05-08-690-495-4	Sequence 4, Appl
7	23	31.3	8.97	4	05-08-899-810-14	Sequence 14, Appl
8	22	22.2	1.888	1	05-09-410-955A-9	Sequence 9, Appl
9	22	22.2	11.0765	4	05-09-132-245A-2	Sequence 2, Appl
10	23	41.3	44.11526	4	05-09-131-842A-1	Sequence 1, Appl
11	22.6	41.3	6.06	2	05-09-819-112-131	Sequence 12, Appl
12	22.6	32.9	9.12	2	05-09-890-55-3	Sequence 3, Appl
13	22.6	42.5	15.68	4	05-09-043-937A-1	Sequence 1, Appl
14	22.6	42.5	4.52	1	05-08-208-036-11	Sequence 11, Appl
15	22.6	42.5	4.52	1	05-08-428-822-11	Sequence 11, Appl
16	22.6	42.5	4.17	2	05-08-513-175-3	Sequence 11, Appl
17	22.4	32.5	2.00	4	05-09-243-415-2	Sequence 3, Appl
18	22.4	32.5	11.90	2	05-08-688-1285-4	Sequence 4, Appl
19	22.4	32.5	11.90	2	05-08-935-445-4	Sequence 4, Appl
20	22.4	42.5	11.90	3	05-08-959-525-4	Sequence 4, Appl
21	22.4	32.5	11.90	3	05-09-098-466-4	Sequence 4, Appl
22	22.4	42.5	11.90	3	05-08-590-988A-4	Sequence 4, Appl
23	22.4	42.5	11.90	3	05-09-053-452-4	Sequence 4, Appl
24	22.4	32.5	11.90	3	05-08-644-115A-4	Sequence 4, Appl
25	22.4	32.5	5.689	6	517197-31	Parent No. 517197
26	22.4	32.5	4.198	2	05-08-431-16-2	Sequence 2, Appl
27	22.2	32.5	12.115	2	05-09-068-562-19	Sequence 19, Appl

28	22.2	32.2	214.4	0.0000	0.0000	0.0000	0.0000	Sequence 14, A411
29	22.2	32.2	266.4	0.0000	0.0000	0.0000	0.0000	Sequence 20, A411
30	22.2	32.2	198.9	0.0000	0.0000	0.0000	0.0000	Sequence 20, A411
41	22	31.9	87.6	0.0000	0.0000	0.0000	0.0000	Sequence 3, A411
42	22	31.9	105.8	0.0000	0.0000	0.0000	0.0000	Sequence 14, A411
43	22	31.9	218.0	0.0000	0.0000	0.0000	0.0000	Sequence 3, A411
44	22	31.9	218.0	0.0000	0.0000	0.0000	0.0000	Sequence 4, A411
45	22	31.9	250.4	0.0000	0.0000	0.0000	0.0000	Sequence 4, A411
46	22	31.9	250.4	0.0000	0.0000	0.0000	0.0000	Sequence 11, A411
47	22	31.9	250.4	0.0000	0.0000	0.0000	0.0000	Sequence 11, A411
48	22	31.9	250.4	0.0000	0.0000	0.0000	0.0000	Sequence 8, A411
49	22	31.9	250.4	0.0000	0.0000	0.0000	0.0000	Sequence 11, A411
40	22	31.9	250.4	0.0000	0.0000	0.0000	0.0000	Sequence 3, A411
41	22	31.9	250.4	0.0000	0.0000	0.0000	0.0000	Sequence 11, A411
42	22	31.9	277.6	0.0000	0.0000	0.0000	0.0000	Sequence 1, A411
43	22	31.9	277.6	0.0000	0.0000	0.0000	0.0000	Sequence 1, A411
44	22	31.9	308.9	0.0000	0.0000	0.0000	0.0000	Sequence 6, A411
45	22	31.9	308.9	0.0000	0.0000	0.0000	0.0000	Sequence 5, A411


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Query Match      44.7% Score 23; DB 1; Length 1288;
Best Local Similarity 47.6%; Pred. No. 11;
Matches 30; Conservative 11; Mismatches 22; Indels 0; Gaps 0

Cy          6  gcaatcctccgagatgaagaacagcctcgaggagggagccaccataaacatattctt 65
              ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          171 KCCWCAACGCGTGGAGATGCTGATGAAAGGAGGAGGAGGAGGAGGAGGAGGAG 250

Oy          66 aga 68
              |||

Db          251 GGA 253

RESULT      9
US-09-103-840A-2
Sequence 2, Affiliation US/09/103/840A
Patient No. 6294328

GENERAL INFORMATION:
APPLICANT: FELSCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: WINTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.000
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

Query Match      33.4% Score 23; DB 4; Length 4403765;
Best Local Similarity 68.1%; Pred. No. 30;
Matches 32; Conservative 0; Mismatches 15; Indels 0; Gaps 0

Cy          5  tgcattcccgttgatgcatatgatgccccctggagggagggccgccacc 51
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Db          407359 tgcattcccgttatgcatatgatgccccctggagggagggccgccacc 407405

RESULT      10
US-09-103-840A-1
Sequence 1, Affiliation US/09/103/840A
Patient No. 6294328

GENERAL INFORMATION:
APPLICANT: FELSCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: WINTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.000
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1
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